AMENDMENTS TO THE CLAIMS

Listing of Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

1 – 59. (**Cancelled**)

60. (**Currently Amended**) A method of identifying compounds that bind to a leukotriene A_4 (LTA_4) hydrolase comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase to form an LTA_4 hydrolase crystal, wherein crystallization is performed as liquid liquid diffusion in a capillary using equal volumes of a buffer: enzyme solution consisting of~~comprising~~:

i) a buffer solution consisting of~~comprising about~~ 28% PEG8000, ~~about~~ 0.1 M Na-acetate, ~~about~~ 0.1 M imidazole at a pH of ~~about~~ 6.8 and with ~~about~~ 5 mM $YbCl_3$ as an additive; and

ii) an enzyme solution consisting of~~comprising about~~ 5 mg/ml LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1 in ~~about~~ 10 mM Tris-HCl at a pH of ~~about~~ 8, supplemented with ~~about~~ 1 mM bestatin;

(b) determining the atomic coordinates of said LTA_4 hydrolase crystal; and

(c) screening the atomic coordinates of a set of candidate compounds against the atomic coordinates of said LTA_4 hydrolase crystal obtained in step a) to identify compounds that bind to the LTA_4 hydrolase;

wherein the crystallization results in a LTA_4 hydrolase crystal having the space group P21212 and the unit cell dimensions a=67.59 Å, b=133.51 Å, and c=83.40 Å and wherein $\alpha=\beta=\gamma=90°$.

61. (**Previously Presented**) The method of claim 60, wherein the LTA_4 hydrolase is purified by adsorption chromatography on hydroxyapatite and anion-exchange chromatography.

62-67. (**Cancelled**)

68. (**Previously Presented**) The method of claim 60, wherein the atomic coordinates of said LTA_4 hydrolase crystal correspond to the atomic coordinates defining atom 1 to atom 4876 as set forth in Table 9.

69. (**Cancelled**)

70. (**Currently Amended**) A method of designing an inhibitor or agonist of LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase to form a crystal and thereafter determining its conformational structure, wherein crystallization is performed as liquid liquid diffusion in a capillary using equal volumes of a buffer: enzyme solution ~~comprising~~consisting of:

i) a buffer solution ~~comprising~~consisting of ~~about~~ 28% PEG8000, ~~about~~ 0.1 M Na-acetate, ~~about~~ 0.1 M imidazole at a pH of ~~about~~ 6.8 and with ~~about~~ 5 mM $YbCl_3$ as an additive; and

ii) an enzyme solution ~~comprising~~consisting of ~~about~~ 5 mg/ml LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1 in ~~about~~ 10 mM Tris-HCl at a pH of ~~about~~ 8, supplemented with ~~about~~ 1 mM bestatin;

(b) identifying at least one compound that is at least in part complementary to the LTA_4 hydrolase by the use of the conformational structure of the crystal complex obtained in step a);

(c) soaking the crystallized LTA_4 hydrolase obtained in step a) with a solution of a compound identified in step b) to obtain a complex of the crystal of said LTA_4 hydrolase and said compound; and

(d) performing X-ray crystallography of the crystal complex of LTA_4 hydrolase and said compound to determine the structure thereof, thereby identifying the compound as an inhibitor or agonist of LTA_4 hydrolase;

wherein the crystallization results in a LTA_4 hydrolase crystal having the space group P21212 and the unit cell dimensions a=67.59 Å, b=133.51 Å, and c=83.40 Å and wherein $\alpha=\beta=\gamma=90^{\circ}$.

71. (**Previously Presented**) The method of claim 70, wherein the LTA_4 hydrolase is purified by adsorption chromatography on hydroxyapatite and anion-exchange chromatography.

72. (**Previously Presented**) The method of claim 70, wherein said compound is an inhibitor of LTA_4 hydrolase.

73-75. (**Cancelled**)

76. (**Previously Presented**) The method of claim 70, wherein the atomic coordinates of said LTA_4 hydrolase crystal correspond to the atomic coordinates defining atom 1 to atom 4876 as set for in Table 9.

77. (**Cancelled**)

78. (**Previously Presented**) The method of claim 70, further comprising the step of refining the structure of said compound obtained in step d) via computer modeling using data obtained from the X-ray crystallography in step d) and repeating steps b)-d).

79. (**Previously Presented**) The method of claim 70, wherein the complex obtained in step c) comprises bestatin.

80-86. (**Cancelled**)